

SEQUENCE LISTING

A



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JAN 05 2001

TECH CENTER 1600/2900

<110> Forschungszentrum Juelich GmbH; Marina Vrlije et al.

<120> Process for the microbial production of amino acids by
boosted activity of export carriers

<130> 1

<140> PCT/DE96/02485

<141> 1996-12-18

<160> 2

<170> PatentIn Ver. 2.0

<210> 1

<211> 2374

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS lysE (Lysin-Exporter)

<222> (1016)...(1726)

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cctgaacctt ttcagaagta actaaggcgc caatccctcg attgctgcat caacgacggc 120

gtctgtgagt ctagctagag atctagattc caggcgccat cgttgccaat acatcggtgt 180

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JAN 10 2001

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FEB 05 2001
TO 1700 MAIL ROOM

TO 1700 MAIL ROOM

gtcaatgggt atctcatcga ggaggatcac ttctctgtgt tttagcatgg gagcagcttg 240
ggtttcggga agaagtcccc aaccaaggcc tcggcgaatt gcctcaccaa aaccttcgc 300
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cgaatctgcg ttgatggcga tggtaacgg gatttcagca agcgtccag atagttgcgc 720
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agctttaacg cgctgactca ccgccgagg ggaaatggaa agggctaagg aggcgccttc 900
gaagctgcct tcatcaatga ttgagagcaa agtgtccagt tgaatgggt tcatgaagct 960
atattaaacc atgttaagaa ccaatcattt tacttaagta cttccatagg tcacg atg 1018

Met

1

gtg atc atg gaa atc ttc att aca ggt ctg ctt ttg ggg gcc agt ctt 1066

Val Ile Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser Leu

5

10

15

tta ctg tcc atc gga ccg cag aat gta ctg gtg att aaa caa gga att 1114

Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly Ile

20

25

30

aag cgc gaa gga ctc att gcg gtt ctt ctc gtg tgt tta att tct gac 1162

Lys Arg Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser Asp

35

40

45

gtc ttt ttg ttc atc gcc ggc acc ttg ggc gtt gat ctt ttg tcc aat 1210

Val Phe Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser Asn

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55

60

65

gcc gcg ccg atc gtg ctc gat att atg cgc tgg ggt ggc atc gct tac 1258

Ala Ala Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala Tyr

70

75

80

ctg tta tgg ttt gcc gtc atg gca gcg aaa gac gcc atg aca aac aag 1306

Leu Leu Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn Lys

85

90

95

gtg gaa gcg cca cag atc att gaa gaa aca gaa cca acc gtg ccc gat 1354

Val Glu Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro Asp

100

105

110

gac acg cct ttg ggc ggt tcg gcg gtg gcc act gac acg cgc aac cgg 1402

Asp Thr Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn Arg

115

120

125

gtg cgg gtg gag gtg agc gtc gat aag cag cgg gtt tgg gta aag ccc 1450
 Val Arg Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys Pro
 130 135 140 145

atg ttg atg gca atc gtg ctg acc tgg ttg aac ccg aat gcg tat ttg 1498
 Met Leu Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr Leu
 150 155 160

gac gcg ttt gtg ttt atc ggc ggc gtc ggc gcg caa tac ggc gac acc 1546
 Asp Ala Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp Thr
 165 170 175

gga cgg tgg att ttc gcc gct ggc gcg ttc gcg gca agc ctg atc tgg 1594
 Gly Arg Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile Trp
 180 185 190

ttc ccg ctg gtg ggt ttc ggc gca gca gca ttg tca cgc ccg ctg tcc 1642
 Phe Pro Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu Ser
 195 200 205

agc ccc aag gtg tgg cgc tgg atc aac gtc gtc gtg gca gtt gtg atg 1690
 Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val Met
 210 215 220 225

acc gca ttg gcc atc aaa ctg atg ttg atg ggt tag ttttcgcggg 1736
 Thr Ala Leu Ala Ile Lys Leu Met Leu Met Gly
 230 235

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tcgcctccaa ctcggcgtca gaaaactcca agttgttgag tgaatcaagg ctgttggtcca 1856

gctgctcaac tgacgaagca ccaatcaatg cactgggtcac ggtatccgcg ccgtactctc 1916
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<210> 2

<211> 236

<212> PRT LysE (Lysin-Exporter)

<213> Corynebacterium glutamicum

<400> 2

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10

15

Leu Leu Leu Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly

20

25

30

Ile	Lys	Arg	Glu	Gly	Leu	Ile	Ala	Val	Leu	Leu	Val	Cys	Leu	Ile	Ser
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Asp	Val	Phe	Leu	Phe	Ile	Ala	Gly	Thr	Leu	Gly	Val	Asp	Leu	Leu	Ser
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Asn	Ala	Ala	Pro	Ile	Val	Leu	Asp	Ile	Met	Arg	Trp	Gly	Gly	Ile	Ala
65						70					75			80	
Tyr	Leu	Leu	Trp	Phe	Ala	Val	Met	Ala	Ala	Lys	Asp	Ala	Met	Thr	Asn
				85						90				95	
Lys	Val	Glu	Ala	Pro	Gln	Ile	Ile	Glu	Glu	Thr	Glu	Pro	Thr	Val	Pro
				100						105				110	
Asp	Asp	Thr	Pro	Leu	Gly	Gly	Ser	Ala	Val	Ala	Thr	Asp	Thr	Arg	Asn
				115						120				125	
Arg	Val	Arg	Val	Glu	Val	Ser	Val	Asp	Lys	Gln	Arg	Val	Trp	Val	Lys
				130						135				140	
Pro	Met	Leu	Met	Ala	Ile	Val	Leu	Thr	Trp	Leu	Asn	Pro	Asn	Ala	Tyr
145						150				155				160	
Leu	Asp	Ala	Phe	Val	Phe	Ile	Gly	Gly	Val	Gly	Ala	Gln	Tyr	Gly	Asp
				165						170				175	
Thr	Gly	Arg	Trp	Ile	Phe	Ala	Ala	Gly	Ala	Phe	Ala	Ala	Ser	Leu	Ile
				180						185				190	
Trp	Phe	Pro	Leu	Val	Gly	Phe	Gly	Ala	Ala	Ala	Leu	Ser	Arg	Pro	Leu
				195						200				205	

Ser Ser Pro Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val

210

215

220

Met Thr Ala Leu Ala Ile Lys Leu Met Leu Met Gly

225

230

235

Q1
Cont



SEQUENCE LISTING

(B)

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<120> Process for the microbial production of amino acids by
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<130> 1

<140> PCT/DE96/02485

<141> 1996-12-18

<160> 3

<170> PatentIn Ver. 2.0

<210> 1

<211> 2374

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS ORF3 (partial)

<222> (2) .. (652)

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<221> CDS LysG (Regulator lyse)

<222> (1421) .. (2293)

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aca gcg gag gcg gct gag ttc atg gcg gag gag ggc tgc ccg ctt ctg				145
Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu				
35	40	45		
att cat cag cca agc tat tcc atc att aat cgt tgg gtg gag gaa ccg				193
Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro				
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ggc gat gac ggt gag aac ttg ttg cag tca gct gcc aac aat ggt ctt				241
Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu				
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Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys				
85	90	95		
tat ctc gat gga att cca gag ggt tcc cgc gcc agc cag ggt aag tcc				337
Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser				
100	105	110		
ctg tct gag ggc atg ttg aac gtg aac aat att gat atg gtc cgc aag				385
Leu Ser Glu Gly Met Leu Asn Val Asn Asn Ile Asp Met Val Arg Lys				
115	120	125		
ctc aat gac atc gcc cag gaa cgc ggg cag tca ctt gcg cag atg gcg				433

Leu Asn Asp Ile Ala Gln Glu Arg Gly Gln Ser Leu Ala Gln Met Ala

130

135

140

ctt gca tgg gtg ctg cgc gag caa gga gag tac ggc gcg gat acc gtg 481

Leu Ala Trp Val Leu Arg Glu Gln Gly Glu Tyr Gly Ala Asp Thr Val

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acc agt gca ttg att ggt gct tcg tca gtt gag cag ctg gac aac agc 529

Thr Ser Ala Leu Ile Gly Ala Ser Ser Val Glu Gln Leu Asp Asn Ser

165

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175

ctt gat tca ctc aac aac ttg gag ttt tct gac gcc gag ttg gag gcg 577

Leu Asp Ser Leu Asn Asn Leu Glu Phe Ser Asp Ala Glu Leu Glu Ala

180

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190

atc gat gag att tcc cac gac gcc ggc atc aac att tgg gcg aag gcc 625

Ile Asp Glu Ile Ser His Asp Ala Gly Ile Asn Ile Trp Ala Lys Ala

195

200

205

acc gat tcc aaa acc cgc gaa aac taa cccatcaaca tcagtttgat 672

Thr Asp Ser Lys Thr Arg Glu Asn

210

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aatcaccagt acattctgcg gtccgatgga cagtaaaaga ctggcccca aaagcagacc 1332

tgtaatgaag atttccatga tcaccatcgt gacctatgga agtacttaag taaaatgatt 1392

ggttcttaac atggtttaat atagcttc atg aac ccc att caa ctg gac act 1444

Met Asn Pro Ile Gln Leu Asp Thr

220

225

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Leu Leu Ser Ile Ile Asp Glu Gly Ser Phe Glu Gly Ala Ser Leu Ala

230

235

240

ctt tcc att tcc ccc tcg gcg gtg agt cag cgc gtt aaa gct ctc gag 1540

Leu Ser Ile Ser Pro Ser Ala Val Ser Gln Arg Val Lys Ala Leu Glu

245

250

255

cat cac gtg ggt cga gtg ttg gta tcg cgc acc caa ccg gcc aaa gca 1588

His His Val Gly Arg Val Leu Val Ser Arg Thr Gln Pro Ala Lys Ala

260

265

270

acc gaa gcg ggt gaa gtc ctt gtg caa gca gcg cgg aaa atg gtg ttg 1636
 Thr Glu Ala Gly Glu Val Leu Val Gln Ala Ala Arg Lys Met Val Leu
 275 280 285

ctg caa gca gaa act aaa gcg caa cta tct gga cgc ctt gct gaa atc 1684
 Leu Gln Ala Glu Thr Lys Ala Gln Leu Ser Gly Arg Leu Ala Glu Ile
 290 295 300 305

ccg tta acc atc gcc atc aac gca gat tcg cta tcc aca tgg ttt cct 1732
 Pro Leu Thr Ile Ala Ile Asn Ala Asp Ser Leu Ser Thr Trp Phe Pro
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ccc gtg ttc aac gag gta gct tct tgg ggt gga gca acg ctc acg ctg 1780
 Pro Val Phe Asn Glu Val Ala Ser Trp Gly Gly Ala Thr Leu Thr Leu
 325 330 335

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 Arg Leu Glu Asp Glu Ala His Thr Leu Ser Leu Leu Arg Arg Gly Asp
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 Val Leu Gly Ala Val Thr Arg Glu Ala Asn Pro Val Ala Gly Cys Glu
 355 360 365

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 Val Val Glu Leu Gly Thr Met Arg His Leu Ala Ile Ala Thr Pro Ser
 370 375 380 385

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 Leu Arg Asp Ala Tyr Met Val Asp Gly Lys Leu Asp Trp Ala Ala Met
 390 395 400

ccc gtc tta cgc ttc ggt ccc aaa gat gtg ctt caa gac cgt gac ctg 2020
 Pro Val Leu Arg Phe Gly Pro Lys Asp Val Leu Gln Asp Arg Asp Leu

405

410

415

gac ggg cgc gtc gat ggt cct gtg ggg cgc agg cgc gta tcc att gtc 2068
 Asp Gly Arg Val Asp Gly Pro Val Gly Arg Arg Arg Val Ser Ile Val

420

425

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ccg tcg gcg gaa ggt ttt ggt gag gca att cgc cga ggc ctt ggt tgg 2116
 Pro Ser Ala Glu Gly Phe Gly Glu Ala Ile Arg Arg Gly Leu Gly Trp

435

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gga ctt ctt ccc gaa acc caa gct gct ccc atg cta aaa gca gga gaa 2164
 Gly Leu Leu Pro Glu Thr Gln Ala Ala Pro Met Leu Lys Ala Gly Glu

450

455

460

465

gtg atc ctc ctc gat gag ata ccc att gac aca ccg atg tat tgg caa 2212
 Val Ile Leu Leu Asp Glu Ile Pro Ile Asp Thr Pro Met Tyr Trp Gln

470

475

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cga tgg cgc ctg gaa tct aga tct cta gct aga ctc aca gac gcc gtc 2260
 Arg Trp Arg Leu Glu Ser Arg Ser Leu Ala Arg Leu Thr Asp Ala Val

485

490

495

gtt gat gca gca atc gag gga ttg cgg cct tag ttactttctga aaaggttcag 2313
 Val Asp Ala Ala Ile Glu Gly Leu Arg Pro

500

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<210> 2

<211> 216

<212> PRT ORF3 (partial)

<213> *Corynebacterium glutamicum*

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Asp Thr Pro Leu Glu Glu Thr Met Tyr Ala Leu Arg Asp Ile Val Ala

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Ser Gly Lys Ala Leu Tyr Val Gly Ile Ser Ser Tyr Gly Pro Glu Leu

20 25 30

Thr Ala Glu Ala Ala Glu Phe Met Ala Glu Glu Gly Cys Pro Leu Leu

35 40 45

Ile His Gln Pro Ser Tyr Ser Ile Ile Asn Arg Trp Val Glu Glu Pro

50 55 60

Gly Asp Asp Gly Glu Asn Leu Leu Gln Ser Ala Ala Asn Asn Gly Leu

65 70 75 80

Gly Val Ile Ala Phe Ser Pro Leu Ala Gln Gly Leu Leu Thr Asp Lys

85 90 95

Tyr Leu Asp Gly Ile Pro Glu Gly Ser Arg Ala Ser Gln Gly Lys Ser

100 105 110

Leu Ser Glu Gly Met Leu Asn Val Asn Asn Ile Asp Met Val Arg Lys

115 120 125

Leu Asn Asp Ile Ala Gln Glu Arg Gly Gln Ser Leu Ala Gln Met Ala

130

135

140

Leu Ala Trp Val Leu Arg Glu Gln Gly Glu Tyr Gly Ala Asp Thr Val

145

150

155

160

Thr Ser Ala Leu Ile Gly Ala Ser Ser Val Glu Gln Leu Asp Asn Ser

165

170

175

Leu Asp Ser Leu Asn Asn Leu Glu Phe Ser Asp Ala Glu Leu Glu Ala

180

185

190

Ile Asp Glu Ile Ser His Asp Ala Gly Ile Asn Ile Trp Ala Lys Ala

195

200

205

Thr Asp Ser Lys Thr Arg Glu Asn

210

215

<210> 3

<211> 290

<212> PRT LysG (Regulator lyse)

<213> Corynebacterium glutamicum

<400> 3

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1

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10

15

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20

25

30

Ser Gln Arg Val Lys Ala Leu Glu His His Val Gly Arg Val Leu Val
 35 40 45

Ser Arg Thr Gln Pro Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val
 50 55 60

Gln Ala Ala Arg Lys Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln
 65 70 75 80

Leu Ser Gly Arg Leu Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala
 85 90 95

Asp Ser Leu Ser Thr Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser
 100 105 110

Trp Gly Gly Ala Thr Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr
 115 120 125

Leu Ser Leu Leu Arg Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu
 130 135 140

Ala Asn Pro Val Ala Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg
 145 150 155 160

His Leu Ala Ile Ala Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp
 165 170 175

Gly Lys Leu Asp Trp Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys
 180 185 190

Asp Val Leu Gln Asp Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val
 195 200 205

Gly Arg Arg Arg Val Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu

210

215

220

Ala Ile Arg Arg Gly Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala

225

230

235

240

Ala Pro Met Leu Lys Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro

245

250

255

Ile Asp Thr Pro Met Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser

260

265

270

Leu Ala Arg Leu Thr Asp Ala Val Val Asp Ala Ala Ile Glu Gly Leu

275

280

285

Arg Pro

290